EDITORIAL Cancer Discovery at One Year: The Editors’ Interim Analysis vi Lewis C. Cantley, PhD, and José Baselga, MD, PhD, Editors-in-Chief

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ONLINE For more News and Research Watch, visit Cancer Discovery online at www.AACR.org/CDnews.

VIEWS In The Spotlight A Role for ATM in Hereditary Pancreatic Cancer 14 J. L. Bakker and J.P. de Winter Commentary on Roberts et al. p. 41


The 14-3-3σ Tumor Suppressor Has Multiple Functions in ErbB2-Induced Breast Cancer 19 N.E. Hynes and T. Smirnova Commentary on Ling et al. p. 68

Tackling Formalin-Fixed, Paraffin-Embedded Tissue with Next-Generation Sequencing 23 C.L. Corless and P.T. Spellman Commentary on Wagle et al. p. 82


Précis: Next-generation sequencing identifies inherited ATM mutations in kindreds with hereditary pancreatic ductal adenocarcinoma.


Précis: Analysis of a donor–recipient pair with follicular lymphoma reveals the time-course of somatic mutations acquired during lymphomagenesis.
OF82
by Targeted, Massively Parallel sequencing
Genomic alterations in clinical Tumor samples
Research Article
Matthew Meyerson     1–3,      Stacey B. Gabriel     3, and      Levi A. Garraway     1–3

Precis: Individualized analyses of the PI3K/AKT and RAS pathways will identify ovarian cancers that may respond to AKT inhibition.

Loss of the 14-3-3σ Tumor Suppressor Is a Critical Event in ErbB2-Mediated Tumor Progression .............................. 68
C. Ling, V-M-T. Su, D. Zuo, and W.J. Muller

Precis: 14-3-3σ inactivation accelerates formation and promotes metastasis of ErbB2/HER2-induced tumors.

For more News and Research Watch, visit Cancer Discovery online at www.AACR.org/CDnews. Online-only News stories include the following:

• Biotech Firms Look for Virtual Success
• "Reversed" Krebs Cycle Can Feed Tumors

• Dual HER2 Blockade Slows Metastatic Breast Cancer
• Modified Stem Cells Create Tumor-Attacking T Cells

Wagle and colleagues describe a method to profile clinically relevant mutations in formalin-fixed, paraffin-embedded tumor samples involving exon capture of frequently mutated or polymorphic genes followed by massively parallel sequencing. This method identifies single-nucleotide variants, insertions, deletions, and copy number alterations overlooked by current genotyping-based methods with high specificity and sensitivity. Identification of such “actionable” genetic alterations that predict response to targeted or conventional cytotoxic therapies has the potential to facilitate individualized cancer treatment in a time- and cost-effective manner. For details, please see the article by Wagle and colleagues on page 82.

High-Throughput Detection of Actionable Genomic Alterations in Clinical Tumor Samples by Targeted, Massively Parallel Sequencing ..................... 82

Precis: Targeted, sequencing-based profiling of archival tumor samples identifies genetic alterations that can direct personalized therapy.